

99-1063-US E1067-20037SEQLIST 81502 Amended.ST25.txt
SEQUENCE LISTING

RECEIVED
TECH CENTER 1600/2900
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<110> O"Mahony, Daniel J
Seveso, Michela

<120> Antibodies To Peptides That Target GIT Receptors And Related
Methods

<130> E1067/20037

<140> US 09/443,780

<141> 1999-11-19

<150> US 60/109,036

<151> 1998-11-19

<160> 84

<170> PatentIn version 3.1

<210> 1

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Random peptide

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Linked to dansyl group

<400> 1

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

<210> 2

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Random peptide

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Linked to dansyl group

<400> 2

Ser	Asp	Asn	Ala	Lys	Glu	Pro	Gly	Asp	Tyr	Asn	Cys	Cys	Gly	Asn	Gly
1				5					10					15	

Asn	Ser	Thr	Gly
			20

<210> 3
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Random peptide

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Linked to dansyl group

C'
<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> D-amino acid

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> D-amino acid

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> D-amino acid

<220>`

<221> MISC_FEATURE

<222> (12)..(13)

<223> D-amino acid

<400> 3

Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro Gly
1 5 10 15

<210> 4

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Random peptide

<400> 4

Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu
1 5 10 15

C1 Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys
20 25 30

Val Phe Asn Arg
35

<210> 5

<211> 29

<212> PRT

<213> Artificial sequence

<220>

<223> Random peptide

<400> 5

Asn Leu Arg Ser Asp Asn Ala Lys Glu Pro Gly Asp Tyr Asn Cys Cys
1 5 10 15

Gly Asn Gly Asn Ser Thr Gly Arg Lys Val Phe Asn Arg
20 25

<210> 6
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Random sequence

<400> 6

Ser Asp Asn Ala Lys Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly
1 5 10 15

Asn Ser Thr Gly
20

<210> 7
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Random peptide

<400> 7

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
1 5 10 15

Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu
20 25 30

Arg Thr Arg Ser Arg Pro Asn Gly
35 40

<210> 8
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Cyclic (internal) random peptide

<400> 8

Thr	Asn	Ala	Lys	His	Ser	Ser	Cys	Asn	Arg	Arg	Leu	Arg	Cys	Arg
1				5					10					15

<210> 9

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Cyclic (internal) random peptide

<400> 9

Thr	Asn	Ala	Lys	His	Ser	Ser	Cys	Asn	Arg	Arg	Cys	Arg	Thr	Arg
1				5					10					15

<210> 10

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Random peptide

<400> 10

Ser	Ala	Arg	Asp	Ser	Gly	Pro	Ala	Glu	Asp	Gly	Ser	Arg	Ala	Val	Arg
1				5					10					15	

Leu	Asn	Gly	Val	Glu	Asn	Ala	Asn	Thr	Arg	Lys	Ser	Ser	Arg	Ser	Asn
			20					25					30		

Pro	Arg	Gly	Arg	Arg	His	Pro	Gly	Gly
		35					40	

<210> 11

<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Random peptide

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> D-amino acid

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> D-amino acid

<400> 11

Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro Gly
1 5 10 15

<210> 12
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Random peptide, D form, retroinversion

<220>
<221> MISC_FEATURE
<222> (1)..(16)
<223> D-amino acid

<400> 12

Gly Pro His Arg Arg Gly Arg Pro Asn Ser Arg Ser Ser Lys Arg Thr
1 5 10 15

<210> 13
<211> 685
<212> PRT
<213> Artificial

<220>

<223> D2H receptor

<400> 13

Met Ala Glu Asp Lys Ser Lys Arg Asp Ser Ile Glu Met Ser Met Lys
1 5 10 15

Gly Cys Gln Thr Asn Asn Gly Phe Val His Asn Glu Asp Ile Leu Glu
20 25 30

Gln Thr Pro Asp Pro Gly Ser Ser Thr Asp Asn Leu Lys His Ser Thr
35 40 45

Arg Gly Ile Leu Gly Ser Gln Glu Pro Asp Phe Lys Gly Val Gln Pro
50 55 60

Tyr Ala Gly Met Pro Lys Glu Val Leu Phe Gln Phe Ser Gly Gln Ala
65 70 75 80

Arg Tyr Arg Ile Pro Arg Glu Ile Leu Phe Trp Leu Thr Val Ala Ser
85 90 95

Val Leu Val Leu Ile Ala Ala Thr Ile Ala Ile Ile Ala Leu Ser Pro
100 105 110

Lys Cys Leu Asp Trp Trp Gln Glu Gly Pro Met Tyr Gln Ile Tyr Pro
115 120 125

Arg Ser Phe Lys Asp Ser Asn Lys Asp Gly Asn Gly Asp Leu Lys Gly
130 135 140

Ile Gln Asp Lys Leu Asp Tyr Ile Thr Ala Leu Asn Ile Lys Thr Val
145 150 155 160

Trp Ile Thr Ser Phe Tyr Lys Ser Ser Leu Lys Asp Phe Arg Tyr Gly
165 170 175

Val Glu Asp Phe Arg Glu Val Asp Pro Ile Phe Gly Thr Met Glu Asp
180 185 190

Phe Glu Asn Leu Val Ala Ala Ile His Asp Lys Gly Leu Lys Leu Ile
195 200 205

Ile Asp Phe Ile Pro Asn His Thr Ser Asp Lys His Ile Trp Phe Gln
210 215 220

Leu Ser Arg Thr Arg Thr Gly Lys Tyr Thr Asp Tyr Tyr Ile Trp His
225 230 235 240

Asp Cys Thr His Glu Asn Gly Lys Thr Ile Pro Pro Asn Asn Trp Leu
245 250 255

Ser Val Tyr Gly Asn Ser Ser Trp His Phe Asp Glu Val Arg Asn Gln
260 265 270

Cys Tyr Phe His Gln Phe Met Lys Glu Gln Pro Asp Leu Asn Phe Arg
275 280 285

Asn Pro Asp Val Gln Glu Glu Ile Lys Glu Ile Leu Arg Phe Trp Leu
290 295 300

Thr Lys Gly Val Asp Gly Phe Ser Leu Asp Ala Val Lys Phe Leu Leu
305 310 315 320

Glu Ala Lys His Leu Arg Asp Glu Ile Gln Val Asn Lys Thr Gln Ile
325 330 335

Pro Asp Thr Val Thr Gln Tyr Ser Glu Leu Tyr His Asp Phe Thr Thr
340 345 350

Thr Gln Val Gly Met His Asp Ile Val Arg Ser Phe Arg Gln Thr Met
355 360 365

Asp Gln Tyr Ser Thr Glu Pro Gly Arg Tyr Arg Phe Met Gly Thr Glu
370 375 380

Ala Tyr Ala Glu Ser Ile Asp Arg Thr Val Met Tyr Tyr Gly Leu Pro
385 390 395 400

Phe Ile Gln Glu Ala Asp Phe Pro Phe Asn Asn Tyr Leu Ser Met Leu
405 410 415

Asp Thr Val Ser Gly Asn Ser Val Tyr Glu Val Ile Thr Ser Trp Met
420 425 430

Glu Asn Met Pro Glu Gly Lys Trp Pro Asn Trp Met Ile Gly Gly Pro
435 440 445

Asp Ser Ser Arg Leu Thr Ser Arg Leu Gly Asn Gln Tyr Val Asn Val
450 455 460

Met Asn Met Leu Leu Phe Thr Leu Pro Gly Thr Pro Ile Thr Tyr Tyr
465 470 475 480

Gly Glu Glu Ile Gly Met Gly Asn Ile Val Ala Ala Asn Leu Asn Glu
485 490 495

Ser Tyr Asp Ile Asn Thr Leu Arg Ser Lys Ser Pro Met Gln Trp Asp
500 505 510

Asn Ser Ser Asn Ala Gly Phe Ser Glu Ala Ser Asn Thr Trp Leu Pro
515 520 525

Thr Asn Ser Asp Tyr His Thr Val Asn Val Asp Val Gln Lys Thr Gln
530 535 540

Pro Arg Ser Ala Leu Lys Leu Tyr Gln Asp Leu Ser Leu Leu His Ala
545 550 555 560

Asn Glu Leu Leu Leu Asn Arg Gly Trp Phe Cys His Leu Arg Asn Asp
565 570 575

Ser His Tyr Val Val Tyr Thr Arg Glu Leu Asp Gly Ile Asp Arg Ile
580 585 590

Phe Ile Val Val Leu Asn Phe Gly Glu Ser Thr Leu Leu Asn Leu His
595 600 605

Asn Met Ile Ser Gly Leu Pro Ala Lys Ile Arg Ile Arg Leu Ser Thr
610 615 620

Asn Ser Ala Asp Lys Gly Ser Lys Val Asp Thr Ser Gly Ile Phe Leu
625 630 635 640

Asp Lys Gly Glu Gly Leu Ile Phe Glu His Asn Thr Lys Asn Leu Leu
645 650 655

His Arg Gln Thr Ala Phe Arg Asp Arg Cys Phe Val Ser Asn Arg Ala
660 665 670

Cys Tyr Ser Ser Val Leu Asn Ile Leu Tyr Thr Ser Cys
675 680 685

<210> 14
<211> 1827
<212> PRT
<213> Artificial

<220>
<223> hSI receptor

<400> 14

Met Ala Arg Lys Lys Phe Ser Gly Leu Glu Ile Ser Leu Ile Val Leu
1 5 10 15

Phe Val Ile Val Thr Ile Ile Ala Ile Ala Leu Ile Val Val Leu Ala
 20 25 30

Thr Lys Thr Pro Ala Val Asp Glu Ile Ser Asp Ser Thr Ser Thr Pro
 35 40 45

Ala Thr Thr Arg Val Thr Thr Asn Pro Ser Asp Ser Gly Lys Cys Pro
 50 55 60

Asn Val Leu Asn Asp Pro Val Asn Val Arg Ile Asn Cys Ile Pro Glu
 65 70 75 80

Gln Phe Pro Thr Glu Gly Ile Cys Ala Gln Arg Gly Cys Cys Trp Arg
 85 90 95

Pro Trp Asn Asp Ser Leu Ile Pro Trp Cys Phe Phe Val Asp Asn His
 100 105 110

Gly Tyr Asn Val Gln Asp Met Thr Thr Thr Ser Ile Gly Val Glu Ala
 115 120 125

Lys Leu Asn Arg Ile Pro Ser Pro Thr Leu Phe Gly Asn Asp Ile Asn
 130 135 140

Ser Val Leu Phe Thr Thr Gln Asn Gln Thr Pro Asn Arg Phe Arg Phe
 145 150 155 160

Lys Ile Thr Asp Pro Asn Asn Arg Arg Tyr Glu Val Pro His Gln Tyr
 165 170 175

Val Lys Glu Phe Thr Gly Pro Thr Val Ser Asp Thr Leu Tyr Asp Val
 180 185 190

Lys Val Ala Gln Asn Pro Phe Ser Ile Gln Val Ile Arg Lys Ser Asn
 195 200 205

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Gly Lys Thr Leu Phe Asp Thr Ser Ile Gly Pro Leu Val Tyr Ser Asp
210 215 220

Gln Tyr Leu Gln Ile Ser Ala Arg Leu Pro Ser Asp Tyr Ile Tyr Gly
225 230 235 240

Ile Gly Glu Gln Val His Lys Arg Phe Arg His Asp Leu Ser Trp Lys
245 250 255

Thr Trp Pro Ile Phe Thr Arg Asp Gln Leu Pro Gly Asp Asn Asn Asn
260 265 270

Asn Leu Tyr Gly His Gln Thr Phe Phe Met Cys Ile Glu Asp Thr Ser
275 280 285

Gly Lys Ser Phe Gly Val Phe Leu Met Asn Ser Asn Ala Met Glu Ile
290 295 300

Phe Ile Gln Pro Thr Pro Ile Val Thr Tyr Arg Val Thr Gly Gly Ile
305 310 315 320

Leu Asp Phe Tyr Ile Leu Leu Gly Asp Thr Pro Glu Gln Val Val Gln
325 330 335

Gln Tyr Gln Gln Leu Val Gly Leu Pro Ala Met Pro Ala Tyr Trp Asn
340 345 350

Leu Gly Phe Gln Leu Ser Arg Trp Asn Tyr Lys Ser Leu Asp Val Val
355 360 365

Lys Glu Val Val Arg Arg Asn Arg Glu Ala Gly Ile Pro Phe Asp Thr
370 375 380

Gln Val Thr Asp Ile Asp Tyr Met Glu Asp Lys Lys Asp Phe Thr Tyr
385 390 395 400

Asp Gln Val Ala Phe Asn Gly Leu Pro Gln Phe Val Gln Asp Leu His
405 410 415

Asp His Gly Gln Lys Tyr Val Ile Ile Leu Asp Pro Ala Ile Ser Ile
420 425 430

Gly Arg Arg Ala Asn Gly Thr Thr Tyr Ala Thr Tyr Glu Arg Gly Asn
435 440 445

Thr Gln His Val Trp Ile Asn Glu Ser Asp Gly Ser Thr Pro Ile Ile
450 455 460

Gly Glu Val Trp Pro Gly Leu Thr Val Tyr Pro Asp Phe Thr Asn Pro
465 470 475 480

Asn Cys Ile Asp Trp Trp Ala Asn Glu Cys Ser Ile Phe His Gln Glu
485 490 495

Val Gln Tyr Asp Gly Leu Trp Ile Asp Met Asn Glu Val Ser Ser Phe
500 505 510

Ile Gln Gly Ser Thr Lys Gly Cys Asn Val Asn Lys Leu Asn Tyr Pro
515 520 525

Pro Phe Thr Pro Asp Ile Leu Asp Lys Leu Met Tyr Ser Lys Thr Ile
530 535 540

Cys Met Asp Ala Val Gln Asn Trp Gly Lys Gln Tyr Asp Val His Ser
545 550 555 560

Leu Tyr Gly Tyr Ser Met Ala Ile Ala Thr Glu Gln Ala Val Gln Lys
565 570 575

Val Phe Pro Asn Lys Arg Ser Phe Ile Leu Thr Arg Ser Thr Phe Ala
580 585 590

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Gly Ser Gly Arg His Ala Ala His Trp Leu Gly Asp Asn Thr Ala Ser
595 600 605

Trp Glu Gln Met Glu Trp Ser Ile Thr Gly Met Leu Glu Phe Ser Leu
610 615 620

Phe Gly Ile Pro Leu Val Gly Ala Asp Ile Cys Gly Phe Val Ala Glu
625 630 635 640

Thr Thr Glu Glu Leu Cys Arg Arg Trp Met Gln Leu Gly Ala Phe Tyr
645 650 655

Pro Phe Ser Arg Asn His Asn Ser Asp Gly Tyr Glu His Gln Asp Pro
660 665 670

Ala Phe Phe Gly Gln Asn Ser Leu Leu Val Lys Ser Ser Arg Gln Tyr
675 680 685

C' Leu Thr Ile Arg Tyr Thr Leu Leu Pro Phe Leu Tyr Thr Leu Phe Tyr
690 695 700

Lys Ala His Val Phe Gly Glu Thr Val Ala Arg Pro Val Leu His Glu
705 710 715 720

Phe Tyr Glu Asp Thr Asn Ser Trp Ile Glu Asp Thr Glu Phe Leu Trp
725 730 735

Gly Pro Ala Leu Leu Ile Thr Pro Val Leu Lys Gln Gly Ala Asp Thr
740 745 750

Val Ser Ala Tyr Ile Pro Asp Ala Ile Trp Tyr Asp Tyr Glu Ser Gly
755 760 765

Ala Lys Arg Pro Trp Arg Lys Gln Arg Val Asp Met Tyr Leu Pro Ala
770 775 780

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Asp Lys Ile Gly Leu His Leu Arg Gly Gly Tyr Ile Ile Pro Ile Gln
785 790 795 800

Glu Pro Asp Val Thr Thr Thr Ala Ser Arg Lys Asn Pro Leu Gly Leu
805 810 815

Ile Val Ala Leu Gly Glu Asn Asn Thr Ala Lys Gly Asp Phe Phe Trp
820 825 830

Asp Asp Gly Glu Thr Lys Asp Thr Ile Gln Asn Gly Asn Tyr Ile Leu
835 840 845

Tyr Thr Phe Ser Val Ser Asn Asn Thr Leu Asp Ile Val Cys Thr His
850 855 860

Ser Ser Tyr Gln Glu Gly Thr Thr Leu Ala Phe Gln Thr Val Lys Ile
865 870 875 880

C' Leu Gly Leu Thr Asp Ser Val Thr Glu Val Arg Val Ala Glu Asn Asn
885 890 895

Gln Pro Met Asn Ala His Ser Asn Phe Thr Tyr Asp Ala Ser Asn Gln
900 905 910

Val Leu Leu Ile Ala Asp Leu Lys Leu Asn Leu Gly Arg Asn Phe Ser
915 920 925

Val Gln Trp Asn Gln Ile Phe Ser Glu Asn Glu Arg Phe Asn Cys Tyr
930 935 940

Pro Asp Ala Asp Leu Ala Thr Glu Gln Lys Cys Thr Gln Arg Gly Cys
945 950 955 960

Val Trp Arg Thr Gly Ser Ser Leu Ser Lys Ala Pro Glu Cys Tyr Phe
965 970 975

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Pro Arg Gln Asp Asn Ser Tyr Ser Val Asn Ser Ala Arg Tyr Ser Ser
980 985 990

Met Gly Ile Thr Ala Asp Leu Gln Leu Asn Thr Ala Asn Ala Arg Ile
995 1000 1005

Lys Leu Pro Ser Asp Pro Ile Ser Thr Leu Arg Val Glu Val Lys
1010 1015 1020

Tyr His Lys Asn Asp Met Leu Gln Phe Lys Ile Tyr Asp Pro Gln
1025 1030 1035

Lys Lys Arg Tyr Glu Val Pro Val Pro Leu Asn Ile Pro Thr Thr
1040 1045 1050

Pro Ile Ser Thr Tyr Glu Asp Arg Leu Tyr Asp Val Glu Ile Lys
1055 1060 1065

Glu Asn Pro Phe Gly Ile Gln Ile Arg Arg Arg Ser Ser Gly Arg
1070 1075 1080

Val Ile Trp Asp Ser Trp Leu Pro Gly Phe Ala Phe Asn Asp Gln
1085 1090 1095

Phe Ile Gln Ile Ser Thr Arg Leu Pro Ser Glu Tyr Ile Tyr Gly
1100 1105 1110

Phe Gly Glu Val Glu His Thr Ala Phe Lys Arg Asp Leu Asn Trp
1115 1120 1125

Asn Thr Trp Gly Met Phe Thr Arg Asp Gln Pro Pro Gly Tyr Lys
1130 1135 1140

Leu Asn Ser Tyr Gly Phe His Pro Tyr Tyr Met Ala Leu Glu Glu
1145 1150 1155

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Glu Gly Asn Ala His Gly Val Phe Leu Leu Asn Ser Asn Ala Met
1160 1165 1170

Asp Val Thr Phe Gln Pro Thr Pro Ala Leu Thr Tyr Arg Thr Val
1175 1180 1185

Gly Gly Ile Leu Asp Phe Tyr Met Phe Leu Gly Pro Thr Pro Gln
1190 1195 1200

Val Ala Thr Lys Gln Tyr His Glu Val Ile Gly His Pro Val Met
1205 1210 1215

Pro Ala Tyr Trp Ala Leu Gly Phe Gln Leu Cys Arg Tyr Gly Tyr
1220 1225 1230

Ala Asn Thr Ser Glu Val Arg Glu Leu Tyr Asp Ala Met Val Ala
1235 1240 1245

Ala Asn Ile Pro Tyr Asp Val Gln Tyr Thr Asp Ile Asp Tyr Met
1250 1255 1260

Glu Arg Gln Leu Asp Phe Thr Ile Gly Glu Ala Phe Gln Asp Leu
1265 1270 1275

Pro Gln Phe Val Asp Lys Ile Arg Gly Glu Gly Met Arg Tyr Ile
1280 1285 1290

Ile Ile Leu Asp Pro Ala Ile Ser Gly Asn Glu Thr Lys Thr Tyr
1295 1300 1305

Pro Ala Phe Glu Arg Gly Gln Gln Asn Asp Val Phe Val Lys Trp
1310 1315 1320

Pro Asn Thr Asn Asp Ile Cys Trp Ala Lys Val Trp Pro Asp Leu
1325 1330 1335

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Pro Asn Ile Thr Ile Asp Lys Thr Leu Thr Glu Asp Glu Ala Val
1340 1345 1350

Asn Ala Ser Arg Ala His Val Ala Phe Pro Asp Phe Phe Arg Thr
1355 1360 1365

Ser Thr Ala Glu Trp Trp Ala Arg Glu Ile Val Asp Phe Tyr Asn
1370 1375 1380

Glu Lys Met Lys Phe Asp Gly Leu Trp Ile Asp Met Asn Glu Pro
1385 1390 1395

Ser Ser Phe Val Asn Gly Thr Thr Thr Asn Gln Cys Arg Asn Asp
1400 1405 1410

Glu Leu Asn Tyr Pro Pro Tyr Phe Pro Glu Leu Thr Lys Arg Thr
1415 1420 1425

Asp Gly Leu His Phe Arg Thr Ile Cys Met Glu Ala Glu Gln Ile
1430 1435 1440

Leu Ser Asp Gly Thr Ser Val Leu His Tyr Asp Val His Asn Leu
1445 1450 1455

Tyr Gly Trp Ser Gln Met Lys Pro Thr His Asp Ala Leu Gln Lys
1460 1465 1470

Thr Thr Gly Lys Arg Gly Ile Val Ile Ser Arg Ser Thr Tyr Pro
1475 1480 1485

Thr Ser Gly Arg Trp Gly Gly His Trp Leu Gly Asp Asn Tyr Ala
1490 1495 1500

Arg Trp Asp Asn Met Asp Lys Ser Ile Ile Gly Met Met Glu Phe
1505 1510 1515

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Ser Leu Phe Gly Ile Ser Tyr Thr Gly Ala Asp Ile Cys Gly Phe
1520 1525 1530

Phe Asn Asn Ser Glu Tyr His Leu Cys Thr Arg Trp Met Gln Leu
1535 1540 1545

Gly Ala Phe Tyr Pro Tyr Ser Arg Asn His Asn Ile Ala Asn Thr
1550 1555 1560

Arg Arg Gln Asp Pro Ala Ser Trp Asn Glu Thr Phe Ala Glu Met
1565 1570 1575

Ser Arg Asn Ile Leu Asn Ile Arg Tyr Thr Leu Leu Pro Tyr Phe
1580 1585 1590

Tyr Thr Gln Met His Glu Ile His Ala Asn Gly Gly Thr Val Ile
1595 1600 1605

Arg Pro Leu Leu His Glu Phe Phe Asp Glu Lys Pro Thr Trp Asp
1610 1615 1620

Ile Phe Lys Gln Phe Leu Trp Gly Pro Ala Phe Met Val Thr Pro
1625 1630 1635

Val Leu Glu Pro Tyr Val Gln Thr Val Asn Ala Tyr Val Pro Asn
1640 1645 1650

Ala Arg Trp Phe Asp Tyr His Thr Gly Lys Asp Ile Gly Val Arg
1655 1660 1665

Gly Gln Phe Gln Thr Phe Asn Ala Ser Tyr Asp Thr Ile Asn Leu
1670 1675 1680

His Val Arg Gly Gly His Ile Leu Pro Cys Gln Glu Pro Ala Gln
1685 1690 1695

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Asn Thr Phe Tyr Ser Arg Gln Lys His Met Lys Leu Ile Val Ala
1700 1705 1710

Ala Asp Asp Asn Gln Met Ala Gln Gly Ser Leu Phe Trp Asp Asp
1715 1720 1725

Gly Glu Ser Ile Asp Thr Tyr Glu Arg Asp Leu Tyr Leu Ser Val
1730 1735 1740

Gln Phe Asn Leu Asn Gln Thr Thr Leu Thr Ser Thr Ile Leu Lys
1745 1750 1755

Arg Gly Tyr Ile Asn Lys Ser Glu Thr Arg Leu Gly Ser Leu His
1760 1765 1770

Val Trp Gly Lys Gly Thr Thr Pro Val Asn Ala Val Thr Leu Thr
1775 1780 1785

Tyr Asn Gly Asn Lys Asn Ser Leu Pro Phe Asn Glu Asp Thr Thr
1790 1795 1800

Asn Met Ile Leu Arg Ile Asp Leu Thr Thr His Asn Val Thr Leu
1805 1810 1815

Glu Glu Pro Ile Glu Ile Asn Trp Ser
1820 1825

<210> 15
<211> 832
<212> PRT
<213> Artificial

<220>
<223> HPT1 receptor

<400> 15

Met Ile Leu Gln Ala His Leu His Ser Leu Cys Leu Leu Met Leu Tyr
1 5 10 15

Leu Ala Thr Gly Tyr Gly Gln Glu Gly Lys Phe Ser Gly Pro Leu Lys
20 25 30

Pro Met Thr Phe Ser Ile Tyr Glu Gly Gln Glu Pro Ser Gln Ile Ile
35 40 45

Phe Gln Phe Lys Ala Asn Pro Pro Ala Val Thr Phe Glu Leu Thr Gly
50 55 60

Glu Thr Asp Asn Ile Phe Val Ile Glu Arg Glu Gly Leu Leu Tyr Tyr
65 70 75 80

Asn Arg Ala Leu Asp Arg Glu Thr Arg Ser Thr His Asn Leu Gln Val
85 90 95

Ala Ala Leu Asp Ala Asn Gly Ile Ile Val Glu Gly Pro Val Pro Ile
100 105 110

Thr Ile Glu Val Lys Asp Ile Asn Asp Asn Arg Pro Thr Phe Leu Gln
115 120 125

Ser Lys Tyr Glu Gly Ser Val Arg Gln Asn Ser Arg Pro Gly Lys Pro
130 135 140

Phe Leu Tyr Val Asn Ala Thr Asp Leu Asp Asp Pro Ala Thr Pro Asn
145 150 155 160

Gly Gln Leu Tyr Tyr Gln Ile Val Ile Gln Leu Pro Met Ile Asn Asn
165 170 175

Val Met Tyr Phe Gln Ile Asn Asn Lys Thr Gly Ala Ile Ser Leu Thr
180 185 190

Arg Glu Gly Ser Gln Glu Leu Asn Pro Ala Lys Asn Pro Ser Tyr Asn
195 200 205

Leu Val Ile Ser Val Lys Asp Met Gly Gly Gln Ser Glu Asn Ser Phe
210 215 220

Ser Asp Thr Thr Ser Val Asp Ile Ile Val Thr Glu Asn Ile Trp Lys
225 230 235 240

Ala Pro Lys Pro Val Glu Met Val Glu Asn Ser Thr Asp Pro His Pro
245 250 255

Ile Lys Ile Thr Gln Val Arg Trp Asn Asp Pro Gly Ala Gln Tyr Ser
260 265 270

Leu Val Asp Lys Glu Lys Leu Pro Arg Phe Pro Phe Ser Ile Asp Gln
275 280 285

Glu Gly Asp Ile Tyr Val Thr Gln Pro Leu Asp Arg Glu Glu Lys Asp
290 295 300

Ala Tyr Val Phe Tyr Ala Val Ala Lys Asp Glu Tyr Gly Lys Pro Leu
305 310 315 320

Ser Tyr Pro Leu Glu Ile His Val Lys Val Lys Asp Ile Asn Asp Asn
325 330 335

Pro Pro Thr Cys Pro Ser Pro Val Thr Val Phe Glu Val Gln Glu Asn
340 345 350

Glu Arg Leu Gly Asn Ser Ile Gly Thr Leu Thr Ala His Asp Arg Asp
355 360 365

Glu Glu Asn Thr Ala Asn Ser Phe Leu Asn Tyr Arg Ile Val Glu Gln
370 375 380

Thr Pro Lys Leu Pro Met Asp Gly Leu Phe Leu Ile Gln Thr Tyr Ala
385 390 395 400

Gly Met Leu Gln Leu Ala Lys Gln Ser Leu Lys Lys Gln Asp Thr Pro
405 410 415

Gln Tyr Asn Leu Thr Ile Glu Val Ser Asp Lys Asp Phe Lys Thr Leu
420 425 430

Cys Phe Val Gln Ile Asn Val Ile Asp Ile Asn Asp Gln Ile Pro Ile
435 440 445

Phe Glu Lys Ser Asp Tyr Gly Asn Leu Thr Leu Ala Glu Asp Thr Asn
450 455 460

Ile Gly Ser Thr Ile Leu Thr Ile Gln Ala Thr Asp Ala Asp Glu Pro
465 470 475 480

Phe Thr Gly Ser Ser Lys Ile Leu Tyr His Ile Ile Lys Gly Asp Ser
485 490 495

C1 Glu Gly Arg Leu Gly Val Asp Thr Asp Pro His Thr Asn Thr Gly Tyr
500 505 510

Val Ile Ile Lys Lys Pro Leu Asp Phe Glu Thr Ala Ala Val Ser Asn
515 520 525

Ile Val Phe Lys Ala Glu Asn Pro Glu Pro Leu Val Phe Gly Val Lys
530 535 540

Tyr Asn Ala Ser Ser Phe Ala Lys Phe Thr Leu Ile Val Thr Asp Val
545 550 555 560

Asn Glu Ala Pro Gln Phe Ser Gln His Val Phe Gln Ala Lys Val Ser
565 570 575

Glu Asp Val Ala Ile Gly Thr Lys Val Gly Asn Val Thr Ala Lys Asp
580 585 590

Pro Glu Gly Leu Asp Ile Ser Tyr Ser Leu Arg Gly Asp Thr Arg Gly
595 600 605

Trp Leu Lys Ile Asp His Val Thr Gly Glu Ile Phe Ser Val Ala Pro
610 615 620

Leu Asp Arg Glu Ala Gly Ser Pro Tyr Arg Val Gln Val Val Ala Thr
625 630 635 640

Glu Val Gly Gly Ser Ser Leu Ser Ser Val Ser Glu Phe His Leu Ile
645 650 655

Leu Met Asp Val Asn Asp Asn Pro Pro Arg Leu Ala Lys Asp Tyr Thr
660 665 670

Gly Leu Phe Phe Cys His Pro Leu Ser Ala Pro Gly Ser Leu Ile Phe
675 680 685

Glu Ala Thr Asp Asp Asp Gln His Leu Phe Arg Gly Pro His Phe Thr
690 695 700

Phe Ser Leu Gly Ser Gly Ser Leu Gln Asn Asp Trp Glu Val Ser Lys
705 710 715 720

Ile Asn Gly Thr His Ala Arg Leu Ser Thr Arg His Thr Asp Phe Glu
725 730 735

Glu Arg Ala Tyr Val Val Leu Ile Arg Ile Asn Asp Gly Gly Arg Pro
740 745 750

Pro Leu Glu Gly Ile Val Ser Leu Pro Val Thr Phe Cys Ser Cys Val
755 760 765

Glu Gly Ser Cys Phe Arg Pro Ala Gly His Gln Thr Gly Ile Pro Thr
770 775 780

Val Gly Met Ala Val Gly Ile Leu Leu Thr Thr Leu Leu Val Ile Gly
785 790 795 800

Ile Ile Leu Ala Val Val Phe Ile Arg Ile Lys Lys Asp Lys Gly Lys
805 810 815

Asp Asn Val Glu Ser Ala Gln Ala Ser Glu Val Lys Pro Leu Arg Ser
820 825 830

<210> 16
<211> 708
<212> PRT
<213> Artificial

<220>
<223> hPEPT1 receptor

<400> 16

Met Gly Met Ser Lys Ser His Ser Phe Phe Gly Tyr Pro Leu Ser Ile
1 5 10 15

Phe Phe Ile Val Val Asn Glu Phe Cys Glu Arg Phe Ser Tyr Tyr Gly
20 25 30

Met Arg Ala Ile Leu Ile Leu Tyr Phe Thr Asn Phe Ile Ser Trp Asp
35 40 45

Asp Asn Leu Ser Thr Ala Ile Tyr His Thr Phe Val Ala Leu Cys Tyr
50 55 60

Leu Thr Pro Ile Leu Gly Ala Leu Ile Ala Asp Ser Trp Leu Gly Lys
65 70 75 80

Phe Lys Thr Ile Val Ser Leu Ser Ile Val Tyr Thr Ile Gly Gln Ala
85 90 95

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Val Thr Ser Val Ser Ser Ile Asn Asp Leu Thr Asp His Asn His Asp
100 105 110

Gly Thr Pro Asp Ser Leu Pro Val His Val Val Leu Ser Leu Ile Gly
115 120 125

Leu Ala Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys Val Ser
130 135 140

Ala Phe Gly Gly Asp Gln Phe Glu Glu Gly Gln Glu Lys Gln Arg Asn
145 150 155 160

Arg Phe Phe Ser Ile Phe Tyr Leu Ala Ile Asn Ala Gly Ser Leu Leu
165 170 175

CI Ser Thr Ile Ile Thr Pro Met Leu Arg Val Gln Gln Cys Gly Ile His
180 185 190

Ser Lys Gln Ala Cys Tyr Pro Leu Ala Phe Gly Val Pro Ala Ala Leu
195 200 205

Met Ala Val Ala Leu Ile Val Phe Val Leu Gly Ser Gly Met Tyr Lys
210 215 220

Lys Phe Lys Pro Gln Gly Asn Ile Met Gly Lys Val Ala Lys Cys Ile
225 230 235 240

Gly Phe Ala Ile Lys Asn Arg Phe Arg His Arg Ser Lys Ala Phe Pro
245 250 255

Lys Arg Glu His Trp Leu Asp Trp Ala Lys Glu Lys Tyr Asp Glu Arg
260 265 270

Leu Ile Ser Gln Ile Lys Met Val Thr Arg Val Met Phe Leu Tyr Ile
275 280 285

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Pro Leu Pro Met Phe Trp Ala Leu Phe Asp Gln Gln Gly Ser Arg Trp
290 295 300

Thr Leu Gln Ala Thr Thr Met Ser Gly Lys Ile Gly Ala Leu Glu Ile
305 310 315 320

Gln Pro Asp Gln Met Gln Thr Val Asn Ala Ile Leu Ile Val Ile Met
325 330 335

Val Pro Ile Phe Asp Ala Val Leu Tyr Pro Leu Ile Ala Lys Cys Gly
340 345 350

Phe Asn Phe Thr Ser Leu Lys Lys Met Ala Val Gly Met Val Leu Ala
355 360 365

Ser Met Ala Phe Val Val Ala Ala Ile Val Gln Val Glu Ile Asp Lys
370 375 380

Thr Leu Pro Val Phe Pro Lys Gly Asn Glu Val Gln Ile Lys Val Leu
385 390 395 400

Asn Ile Gly Asn Asn Thr Met Asn Ile Ser Leu Pro Gly Glu Met Val
405 410 415

Thr Leu Gly Pro Met Ser Gln Thr Asn Ala Phe Met Thr Phe Asp Val
420 425 430

Asn Lys Leu Thr Arg Ile Asn Ile Ser Ser Pro Gly Ser Pro Val Thr
435 440 445

Ala Val Thr Asp Asp Phe Lys Gln Gly Gln Arg His Thr Leu Leu Val
450 455 460

Trp Ala Pro Asn His Tyr Gln Val Val Lys Asp Gly Leu Asn Gln Lys
465 470 475 480

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Pro Glu Lys Gly Glu Asn Gly Ile Arg Phe Val Asn Thr Phe Asn Glu
485 490 495

Leu Ile Thr Ile Thr Met Ser Gly Lys Val Tyr Ala Asn Ile Ser Ser
500 505 510

Tyr Asn Ala Ser Thr Tyr Gln Phe Phe Pro Ser Gly Ile Lys Gly Phe
515 520 525

Thr Ile Ser Ser Thr Glu Ile Pro Pro Gln Cys Gln Pro Asn Phe Asn
530 535 540

Thr Phe Tyr Leu Glu Phe Gly Ser Ala Tyr Thr Tyr Ile Val Gln Arg
545 550 555 560

Lys Asn Asp Ser Cys Pro Glu Val Lys Val Phe Glu Asp Ile Ser Ala
565 570 575

Asn Thr Val Asn Met Ala Leu Gln Ile Pro Gln Tyr Phe Leu Leu Thr
580 585 590

Cys Gly Glu Val Val Phe Ser Val Thr Gly Leu Glu Phe Ser Tyr Ser
595 600 605

Gln Ala Pro Ser Asn Met Lys Ser Val Leu Gln Ala Gly Trp Leu Leu
610 615 620

Thr Val Ala Val Gly Asn Ile Ile Val Leu Ile Val Ala Gly Ala Gly
625 630 635 640

Gln Phe Ser Lys Gln Trp Ala Glu Tyr Ile Leu Phe Ala Ala Leu Leu
645 650 655

Leu Val Val Cys Val Val Phe Ala Ile Met Ala Arg Phe Tyr Thr Tyr
660 665 670

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Ile Asn Pro Ala Glu Ile Glu Ala Gln Phe Asp Glu Asp Glu Lys Lys
675 680 685

Asn Arg Leu Glu Lys Ser Asn Pro Tyr Phe Met Ser Gly Ala Asn Ser
690 695 700

Gln Lys Gln Met
705

<210> 17
<211> 44
<212> PRT
<213> Artificial

<220>
<223> S15 44 mer fragment L-form

<400> 17

Arg Ser Gly Ala Tyr Glu Ser Pro Asp Gly Arg Gly Gly Arg Ser Tyr
1 5 10 15

Val Gly Gly Gly Gly Gly Cys Gly Asn Ile Gly Arg Lys His Asn Leu
20 25 30

Trp Gly Leu Arg Thr Ala Ser Pro Ala Cys Trp Asp
35 40

<210> 18
<211> 44
<212> PRT
<213> Artificial

<220>
<223> S21 44 mer fragment L-form

<400> 18

Ser Pro Arg Ser Phe Trp Pro Val Val Ser Arg His Glu Ser Phe Gly
1 5 10 15

Ile Ser Asn Tyr Leu Gly Cys Gly Tyr Arg Thr Cys Ile Ser Gly Thr
 20 25 30

Met Thr Lys Ser Ser Pro Ile Tyr Pro Arg His Ser
 35 40

<210> 19
 <211> 44
 <212> PRT
 <213> Artificial

<220>
 <223> S22 44 mer fragment L-form

<400> 19

Ser Ser Ser Ser Asp Trp Gly Gly Val Pro Gly Lys Val Val Arg Glu
 1 5 10 15

Arg Phe Lys Gly Arg Gly Cys Gly Ile Ser Ile Thr Ser Val Leu Thr
 20 25 30

Gly Lys Pro Asn Pro Cys Pro Glu Pro Lys Ala Ala
 35 40

<210> 20
 <211> 44
 <212> PRT
 <213> Artificial

<220>
 <223> Sni10 44 mer fragment L-form

<400> 20

Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg
 1 5 10 15

Ser Cys Ala His Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His Gly
 20 25 30

Cys Ile Thr Arg Pro Leu Arg Gln Ala Ser Ala His
 35 40

<210> 21
 <211> 39
 <212> PRT
 <213> Artificial

<220>
 <223> Sni28 39 mer fragment L-form

<400> 21

Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu
 1 5 10 15

Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr Pro
 20 25 30

C1 Gln Leu Pro Arg Gly Pro Asn
 35

<210> 22
 <211> 41
 <212> PRT
 <213> Artificial

<220>
 <223> Sni34 41 mer fragment L-form

<400> 22

Ser Pro Cys Gly Gly Ser Trp Gly Arg Phe Met Gln Gly Gly Leu Phe
 1 5 10 15

Gly Gly Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg Thr Ser Ala
 20 25 30

Ser Leu Glu Pro Pro Ser Ser Asp Tyr
 35 40

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<210> 23
<211> 39
<212> PRT
<213> Artificial

<220>
<223> Sni38 39 mer fragment L-form

<400> 23

Arg Gly Ala Ala Asp Gln Arg Arg Gly Trp Ser Glu Asn Leu Gly Leu
1 5 10 15

Pro Arg Val Gly Trp Asp Ala Ile Ala His Asn Ser Tyr Thr Phe Thr
20 25 30

Ser Arg Arg Pro Arg Pro Pro
35

C1
<210> 24
<211> 44
<212> PRT
<213> Artificial

<220>
<223> Sni45 44 mer fragment L-form

<400> 24

Ser Gly Gly Glu Val Ser Ser Trp Gly Arg Val Asn Asp Leu Cys Ala
1 5 10 15

Arg Val Ser Trp Thr Gly Cys Gly Thr Ala Arg Ser Ala Arg Thr Asp
20 25 30

Asn Lys Gly Phe Leu Pro Lys His Ser Ser Leu Arg
35 40

<210> 25
<211> 44
<212> PRT
<213> Artificial

<220>

<223> SniAX2 44 mer fragment L-form

<400> 25

Ser Asp Ser Asp Gly Asp His Tyr Gly Leu Arg Gly Gly Val Arg Cys
1 5 10 15

Ser Leu Arg Asp Arg Gly Cys Gly Leu Ala Leu Ser Thr Val His Ala
20 25 30

Gly Pro Pro Ser Phe Tyr Pro Lys Leu Ser Ser Pro
35 40

<210> 26

<211> 39

<212> PRT

<213> Artificial

<220>

<223> SniAX4 39 mer fragment L-form

<400> 26

Arg Ser Leu Gly Asn Tyr Gly Val Thr Gly Thr Val Asp Val Thr Val
1 5 10 15

Leu Pro Met Pro Gly His Ala Asn His Leu Gly Val Ser Ser Ala Ser
20 25 30

Ser Ser Asp Pro Pro Arg Arg
35

<210> 27

<211> 38

<212> PRT

<213> Artificial

<220>

<223> SniAX6 38 mer fragment L-form

<400> 27

Arg Thr Thr Thr Ala Lys Gly Cys Leu Leu Gly Ser Phe Gly Val Leu
1 5 10 15

Ser Gly Cys Ser Phe Thr Pro Thr Ser Pro Pro Pro His Leu Gly Tyr
20 25 30

Pro Pro His Ser Val Asn
35

<210> 28

<211> 39

<212> PRT

<213> Artificial

<220>

<223> SniAX8 39 mer fragment L-form

<400> 28

Ser Pro Lys Leu Ser Ser Val Gly Val Met Thr Lys Val Thr Glu Leu
1 5 10 15

Pro Thr Glu Gly Pro Asn Ala Ile Ser Ile Pro Ile Ser Ala Thr Leu
20 25 30

Gly Pro Arg Asn Pro Leu Arg
35

<210> 29

<211> 39

<212> PRT

<213> Artificial

<220>

<223> DAB3 39 mer fragment L-form

<400> 29

Arg Trp Cys Gly Ala Glu Leu Cys Asn Ser Val Thr Lys Lys Phe Arg
1 5 10 15

Pro Gly Trp Arg Asp His Ala Asn Pro Ser Thr His His Arg Thr Pro
20 25 30

Pro Pro Ser Gln Ser Ser Pro
35

<210> 30
<211> 44
<212> PRT
<213> Artificial

<220>
<223> DAB7 44 mer fragment L-form

<400> 30

Arg Trp Cys Gly Ala Asp Asp Pro Cys Gly Ala Ser Arg Trp Arg Gly
1 5 10 15

Gly Asn Ser Leu Phe Gly Cys Gly Leu Arg Cys Ser Ala Ala Gln Ser
20 25 30

Thr Pro Ser Gly Arg Ile His Ser Thr Ser Thr Ser
35 40

<210> 31
<211> 39
<212> PRT
<213> Artificial

<220>
<223> DAB10 39 mer fragment L-form

<400> 31

Ser Lys Ser Gly Glu Gly Gly Asp Ser Ser Arg Gly Glu Thr Gly Trp
1 5 10 15

Ala Arg Val Arg Ser His Ala Met Thr Ala Gly Arg Phe Arg Trp Tyr
20 25 30

Asn Gln Leu Pro Ser Asp Arg
35

<210> 32
<211> 38
<212> PRT
<213> Artificial

<220>
<223> DAB18 38 mer fragment L-form

<400> 32

Arg Ser Ser Ala Asn Asn Cys Glu Trp Lys Ser Asp Trp Met Arg Arg
1 5 10 15

Ala Cys Ile Ala Arg Tyr Ala Asn Ser Ser Gly Pro Ala Arg Ala Val
20 25 30

Asp Thr Lys Ala Ala Pro
35

<210> 33
<211> 44
<212> PRT
<213> Artificial

<220>
<223> DAB24 44 mer fragment L-form

<400> 33

Ser Lys Trp Ser Trp Ser Ser Arg Trp Gly Ser Pro Gln Asp Lys Val
1 5 10 15

Glu Lys Thr Arg Ala Gly Cys Gly Gly Ser Pro Ser Ser Thr Asn Cys
20 25 30

His Pro Tyr Thr Phe Ala Pro Pro Pro Gln Ala Gly
35 40

<210> 34
 <211> 44
 <212> PRT
 <213> Artificial

<220>
 <223> DAB30 44 mer fragment L-form

<400> 34

Ser Gly Phe Trp Glu Phe Ser Arg Gly Leu Trp Asp Gly Glu Asn Arg
 1 5 10 15

Lys Ser Val Arg Ser Gly Cys Gly Phe Arg Gly Ser Ser Ala Gln Gly
 20 25 30

Pro Cys Pro Val Thr Pro Ala Thr Ile Asp Lys His
 35 40

<210> 35
 <211> 44
 <212> PRT
 <213> Artificial

<220>
 <223> DAX15 44 mer fragment L-form

<400> 35

Ser Glu Ser Gly Arg Cys Arg Ser Val Ser Arg Trp Met Thr Thr Trp
 1 5 10 15

Gln Thr Gln Lys Gly Gly Cys Gly Ser Asn Val Ser Arg Gly Ser Pro
 20 25 30

Leu Asp Pro Ser His Gln Thr Gly His Ala Thr Thr
 35 40

<210> 36
 <211> 39

<212> PRT

<213> Artificial

<220>

<223> DAX23 39 mer fragment L-form

<400> 36

Arg Glu Trp Arg Phe Ala Gly Pro Pro Leu Asp Leu Trp Ala Gly Pro
1 5 10 15

Ser Leu Pro Ser Phe Asn Ala Ser Ser His Pro Arg Ala Leu Arg Thr
20 25 30

Tyr Trp Ser Gln Arg Pro Arg
35

<210> 37

<211> 44

<212> PRT

<213> Artificial

<220>

<223> DAX24 44 mer fragment L-form

<400> 37

Arg Met Glu Asp Ile Lys Asn Ser Gly Trp Arg Asp Ser Cys Arg Trp
1 5 10 15

Gly Asp Leu Arg Pro Gly Cys Gly Ser Arg Gln Trp Tyr Pro Ser Asn
20 25 30

Met Arg Ser Ser Arg Asp Tyr Pro Ala Gly Gly His
35 40

<210> 38

<211> 36

<212> PRT

<213> Artificial

<220>

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<223> DAX27 36 mer fragment L-form

<400> 38

Ser His Pro Trp Tyr Arg His Trp Asn His Gly Asp Phe Ser Gly Ser
1 5 10 15

Gly Gln Ser Arg His Thr Pro Pro Glu Ser Pro His Pro Gly Arg Pro
20 25 30

Asn Ala Thr Ile
35

C1
<210> 39
<211> 44
<212> PRT
<213> Artificial

<220>
<223> DCX8 44 mer fragment L-form

<400> 39

Arg Tyr Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser
1 5 10 15

Ser Ser Val Arg Gly Gly Cys Gly Ala His Ser Ser Pro Pro Arg Ala
20 25 30

Gly Arg Gly Pro Arg Gly Thr Met Val Ser Arg Leu
35 40

<210> 40
<211> 44
<212> PRT
<213> Artificial

<220>
<223> DCX11 44 mer fragment L-form

<400> 40

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Ser Gln Gly Ser Lys Gln Cys Met Gln Tyr Arg Thr Gly Arg Leu Thr
1 5 10 15

Val Gly Ser Glu Tyr Gly Cys Gly Met Asn Pro Ala Arg His Ala Thr
20 25 30

Pro Ala Tyr Pro Ala Arg Leu Leu Pro Arg Tyr Arg
35 40

<210> 41

<211> 44

<212> PRT

<213> Artificial

<220>

<223> DCX26 44 mer fragment L-form

<400> 41

Ser Gly Arg Thr Thr Ser Glu Ile Ser Gly Leu Trp Gly Trp Gly Asp
1 5 10 15

Asp Arg Ser Gly Tyr Gly Trp Gly Asn Thr Leu Arg Pro Asn Tyr Ile
20 25 30

Pro Tyr Arg Gln Ala Thr Asn Arg His Arg Tyr Thr
35 40

<210> 42

<211> 39

<212> PRT

<213> Artificial

<220>

<223> DCX33 39 mer fragment L-form

<400> 42

Arg Trp Asn Trp Thr Val Leu Pro Ala Thr Gly Gly His Tyr Trp Thr
1 5 10 15

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Arg Ser Thr Asp Tyr His Ala Ile Asn Asn His Arg Pro Ser Ile Pro
20 25 30

His Gln His Pro Thr Pro Ile
35

<210> 43
<211> 44
<212> PRT
<213> Artificial

<220>
<223> DCX36 44 mer fragment L-form

<400> 43

Ser Trp Ser Ser Trp Asn Trp Ser Ser Lys Thr Thr Arg Leu Gly Asp
1 5 10 15

Arg Ala Thr Arg Glu Gly Cys Gly Pro Ser Gln Ser Asp Gly Cys Pro
20 25 30

Tyr Asn Gly Arg Leu Thr Thr Val Lys Pro Arg Thr
35 40

<210> 44
<211> 37
<212> PRT
<213> Artificial

<220>
<223> DCX39 37 mer fragment L-form

<400> 44

Ser Gly Ser Leu Asn Ala Trp Gln Pro Arg Ser Trp Val Gly Gly Ala
1 5 10 15

Phe Arg Ser His Ala Asn Asn Asn Leu Asn Pro Lys Pro Thr Met Val
20 25 30

99-1063-US E1067-20037SEQLST 81502 Amended.ST25.txt
Thr Arg His Pro Thr
35

<210> 45
<211> 44
<212> PRT
<213> Artificial

<220>
<223> DCX42 44 mer fragment L-form

<400> 45

Arg Tyr Ser Gly Leu Ser Pro Arg Asp Asn Gly Pro Ala Cys Ser Gln
1 5 10 15

Glu Ala Thr Leu Glu Gly Cys Gly Ala Gln Arg Leu Met Ser Thr Arg
20 25 30

Arg Lys Gly Arg Asn Ser Arg Pro Gly Trp Thr Leu
35 40

<210> 46
<211> 39
<212> PRT
<213> Artificial

<220>
<223> DCX45 39 mer fragment L-form

<400> 46

Ser Val Gly Asn Asp Lys Thr Ser Arg Pro Val Ser Phe Tyr Gly Arg
1 5 10 15

Val Ser Asp Leu Trp Asn Ala Ser Leu Met Pro Lys Arg Thr Pro Ser
20 25 30

Ser Lys Arg His Asp Asp Gly
35

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<210> 47
<211> 38
<212> PRT
<213> Artificial

<220>
<223> PAX9 38 mer fragment L-form

<400> 47

Arg Trp Pro Ser Val Gly Tyr Lys Gly Asn Gly Ser Asp Thr Ile Asp
1 5 10 15

Val His Ser Asn Asp Ala Ser Thr Lys Arg Ser Leu Ile Tyr Asn His
20 25 30

Arg Arg Pro Leu Phe Pro
35

<210> 48
<211> 39
<212> PRT
<213> Artificial

<220>
<223> PAX14 39 mer fragment L-form

<400> 48

Arg Thr Phe Glu Asn Asp Gly Leu Gly Val Gly Arg Ser Ile Gln Lys
1 5 10 15

Lys Ser Asp Arg Trp Tyr Ala Ser His Asn Ile Arg Ser His Phe Ala
20 25 30

Ser Met Ser Pro Ala Gly Lys
35

<210> 49
<211> 44
<212> PRT
<213> Artificial

<220>

<223> PAX15 44 mer fragment L-form

<400> 49

Ser Tyr Cys Arg Val Lys Gly Gly Gly Glu Gly Gly His Thr Asp Ser
1 5 10 15

Asn Leu Ala Arg Ser Gly Cys Gly Lys Val Ala Arg Thr Ser Arg Leu
20 25 30

Gln His Ile Asn Pro Arg Ala Thr Pro Pro Ser Arg
35 40

<210> 50

<211> 39

<212> PRT

<213> Artificial

<220>

<223> PAX16 39 mer fragment L-form

<400> 50

Ser Trp Thr Arg Trp Gly Lys His Thr His Gly Gly Phe Val Asn Lys
1 5 10 15

Ser Pro Pro Gly Lys Asn Ala Thr Ser Pro Tyr Thr Asp Ala Gln Leu
20 25 30

Pro Ser Asp Gln Gly Pro Pro
35

<210> 51

<211> 44

<212> PRT

<213> Artificial

<220>

<223> PAX17 44 mer fragment L-form

99-1063-US E1067-20037SEQLST 81502 Amended.ST25.txt
<400> 51

Ser Gln Val Asp Ser Phe Arg Asn Ser Phe Arg Trp Tyr Glu Pro Ser
1 5 10 15

Arg Ala Leu Cys His Gly Cys Gly Lys Arg Asp Thr Ser Thr Thr Arg
20 25 30

Ile His Asn Ser Pro Ser Asp Ser Tyr Pro Thr Arg
35 40

<210> 52
<211> 39
<212> PRT
<213> Artificial

<220>
<223> PAX18 39 mer fragment L-form

<400> 52

Ser Phe Leu Arg Phe Gln Ser Pro Arg Phe Glu Asp Tyr Ser Arg Thr
1 5 10 15

Ile Ser Arg Leu Arg Asn Ala Thr Asn Pro Ser Asn Val Ser Asp Ala
20 25 30

His Asn Asn Arg Ala Leu Ala
35

<210> 53
<211> 39
<212> PRT
<213> Artificial

<220>
<223> PAX35 39 mer fragment L-form

<400> 53

Arg Ser Ile Thr Asp Gly Gly Leu Asn Glu Val Asp Leu Ser Ser Val
1 5 10 15

Ser Asn Val Leu Glu Asn Ala Asn Ser His Arg Ala Tyr Arg Lys His
20 25 30

Arg Pro Thr Leu Lys Arg Pro
35

<210> 54
<211> 44
<212> PRT
<213> Artificial

<220>
<223> PAX38 44 mer fragment L-form

<400> 54

Ser Ser Lys Val Ser Ser Pro Arg Asp Pro Thr Val Pro Arg Lys Gly
1 5 10 15

Gly Asn Val Asp Tyr Gly Cys Gly His Arg Ser Ser Ala Arg Met Pro
20 25 30

CI Thr Ser Ala Leu Ser Ser Ile Thr Lys Cys Tyr Thr
35 40

<210> 55
<211> 44
<212> PRT
<213> Artificial

<220>
<223> PAX40 44 mer fragment L-form

<400> 55

Arg Ala Ser Thr Gln Gly Gly Arg Gly Val Ala Pro Glu Phe Gly Ala
1 5 10 15

Ser Val Leu Gly Arg Gly Cys Gly Ser Ala Thr Tyr Tyr Thr Asn Ser
20 25 30

Thr Ser Cys Lys Asp Ala Met Gly His Asn Tyr Ser
35 40

<210> 56
<211> 39
<212> PRT
<213> Artificial

<220>
<223> PAX43 39 mer fragment L-form

<400> 56

Arg Trp Cys Glu Lys His Lys Phe Thr Ala Ala Arg Cys Ser Ala Gly
1 5 10 15

Ala Gly Phe Glu Arg Asp Ala Ser Arg Pro Pro Gln Pro Ala His Arg
20 25 30

Asp Asn Thr Asn Arg Asn Ala
35

<210> 57
<211> 39
<212> PRT
<213> Artificial

<220>
<223> PAX45 39 mer fragment L-form

<400> 57

Ser Phe Gln Val Tyr Pro Asp His Gly Leu Glu Arg His Ala Leu Asp
1 5 10 15

Gly Thr Gly Pro Leu Tyr Ala Met Pro Gly Arg Trp Leu Arg Ala Arg
20 25 30

Pro Gln Asn Arg Asp Arg Gln
35

<210> 58
<211> 38
<212> PRT
<213> Artificial

<220>
<223> PAX46 38 mer fragment L-form

<400> 58

Ser Arg Cys Thr Asp Asn Glu Gln Cys Pro Asp Thr Gly Thr Arg Ser
1 5 10 15

Arg Ser Val Ser Asn Ala Arg Tyr Phe Ser Ser Arg Leu Leu Lys Thr
20 25 30

His Ala Pro His Arg Pro
35

cr
<210> 59
<211> 39
<212> PRT
<213> Artificial

<220>
<223> P31 39 mer fragment L-form

<400> 59

Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg
1 5 10 15

Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn
20 25 30

Pro Arg Gly Arg Arg His Pro
35

<210> 60
<211> 44

99-1063-US E1067-20037SEQ LST 81502 Amended.ST25.txt

<212> PRT

<213> Artificial

<220>

<223> P90 44 mer fragment L-form

<400> 60

Ser Ser Ala Asp Ala Glu Lys Cys Ala Gly Ser Leu Leu Trp Trp Gly
1 5 10 15

Arg Gln Asn Asn Ser Gly Cys Gly Ser Pro Thr Lys Lys His Leu Lys
20 25 30

His Arg Asn Arg Ser Gln Thr Ser Ser Ser Ser His
35 40

<210> 61

<211> 39

<212> PRT

<213> Artificial

<220>

<223> 5PAX3 39 mer fragment L-form

<400> 61

Arg Pro Lys Asn Val Ala Asp Ala Tyr Ser Ser Gln Asp Gly Ala Ala
1 5 10 15

Ala Glu Glu Thr Ser His Ala Ser Asn Ala Ala Arg Lys Ser Pro Lys
20 25 30

His Lys Pro Leu Arg Arg Pro
35

<210> 62

<211> 39

<212> PRT

<213> Artificial

<220>

99-1063-US E1067-20037SEQLIST 81502 Amended.ST25.txt
<223> 5PAX5 39 mer fragment L-form

<400> 62

Arg Gly Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu Asn
1 5 10 15

Leu His Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp Tyr
20 25 30

Pro Ser Asn Arg Gly His Lys
35

<210> 63

<211> 39

<212> PRT

<213> Artificial

<220>

<223> 5PAX7 39 mer fragment L-form

<400> 63

Arg Trp Gly Trp Glu Arg Ser Pro Ser Asp Tyr Asp Ser Asp Met Asp
1 5 10 15

Leu Gly Ala Arg Arg Tyr Ala Thr Arg Thr His Arg Ala Pro Pro Arg
20 25 30

Val Leu Lys Ala Pro Leu Pro
35

<210> 64

<211> 44

<212> PRT

<213> Artificial

<220>

<223> 5PAX12 44 mer fragment L-form

<400> 64

99-1063-US E1067-20037SEQLIST 81502 Amended.ST25.txt

Arg Gly Trp Lys Cys Glu Gly Ser Gln Ala Ala Tyr Gly Asp Lys Asp
1 5 10 15

Ile Gly Arg Ser Arg Gly Cys Gly Ser Ile Thr Lys Asn Asn Thr Asn
20 25 30

His Ala His Pro Ser His Gly Ala Val Ala Lys Ile
35 40

<210> 65
<211> 39
<212> PRT
<213> Artificial

<220>
<223> HAX9 39 mer fragment L-form

<400> 65

C1 Ser Arg Glu Glu Ala Asn Trp Asp Gly Tyr Lys Arg Glu Met Ser His
1 5 10 15

Arg Ser Arg Phe Trp Asp Ala Thr His Leu Ser Arg Pro Arg Arg Pro
20 25 30

Ala Asn Ser Gly Asp Pro Asn
35

<210> 66
<211> 44
<212> PRT
<213> Artificial

<220>
<223> HAX35 44 mer fragment L-form

<400> 66

Glu Trp Tyr Ser Trp Lys Arg Ser Ser Lys Ser Thr Gly Leu Gly Asp
1 5 10 15

Thr Ala Thr Arg Glu Gly Cys Gly Pro Ser Gln Ser Asp Gly Cys Pro
20 25 30

Tyr Asn Gly Arg Leu Thr Thr Val Lys Pro Arg Lys
35 40

<210> 67
<211> 44
<212> PRT
<213> Artificial

<220>
<223> HAX40 44 mer fragment L-form

<400> 67

Arg Glu Phe Ala Glu Arg Arg Leu Trp Gly Cys Asp Asp Leu Ser Trp
1 5 10 15

Arg Leu Asp Ala Glu Gly Cys Gly Pro Thr Pro Ser Asn Arg Ala Val
20 25 30

Lys His Arg Lys Pro Arg Pro Arg Ser Pro Ala Leu
35 40

<210> 68
<211> 44
<212> PRT
<213> Artificial

<220>
<223> HAX42 44 mer fragment L-form

<400> 68

Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu
1 5 10 15

Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys
20 25 30

99-1063-US E1067-20037SEQLIST 81502 Amended.ST25.txt
Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
35 40

<210> 69
<211> 44
<212> PRT
<213> Artificial

<220>
<223> HCA3 44 mer fragment L-form

<400> 69

Arg His Ile Ser Glu Tyr Ser Phe Ala Asn Ser His Leu Met Gly Gly
1 5 10 15

Glu Ser Lys Arg Lys Gly Cys Gly Ile Asn Gly Ser Phe Ser Pro Thr
20 25 30

Cys Pro Arg Ser Pro Thr Pro Ala Phe Arg Arg Thr
35 40

C1
<210> 70
<211> 38
<212> PRT
<213> Artificial

<220>
<223> H40 38 mer fragment L-form

<400> 70

Ser Arg Glu Ser Gly Met Trp Gly Ser Trp Trp Arg Gly His Arg Leu
1 5 10 15

Asn Ser Thr Gly Gly Asn Ala Asn Met Asn Ala Ser Leu Pro Pro Asp
20 25 30

Pro Pro Val Ser Thr Pro
35

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<210> 71

<211> 39

<212> PRT

<213> Artificial

<220>

<223> PAX2 39 mer fragment L-form

<400> 71

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
1 5 10 15

Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu
20 25 30

Arg Thr Arg Ser Arg Pro Asn
35

<210> 72

<211> 11

<212> PRT

<213> Artificial

<220>

<223> binding 11 mer fragment L-form

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> "X=S or T"

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> "X= R or K"

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> "X= K or R"

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> "X= S or L"

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> "X= R,I,V or S "

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> "X= S, Y, F, or H "

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> "X=F, H or R "

<400> 72

Xaa Thr Xaa Xaa Ser Xaa Xaa Xaa Asn Xaa Arg
1 5 10

<210> 73

<211> 8

<212> PRT

<213> Artificial

<220>

<223> binding 8 mer fragment L-form

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> "X=S,A or G"

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> "X=V or Q"

<220>
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<222> (7)..(7)
<223> "X = P, G or S"

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> "X = W or Y"

<400> 73

Asp Xaa Asp Xaa Arg Arg Xaa Xaa
1 5

<210> 74
<211> 10
<212> PRT
<213> Artificial

<220>
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<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> "X = A or F"

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> "X = R or H"

<400> 74

Val Arg Ser Gly Cys Gly Xaa Xaa Ser Ser
1 5 10

<210> 75
<211> 11

<212> PRT

<213> Artificial

<220>

<223> binding 11 mer fragment L-form

<400> 75

Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg
1 5 10

<210> 76

<211> 11

<212> PRT

<213> Artificial

<220>

<223> binding 11 mer fragment L-form

<400> 76

Ser Thr Lys Arg Ser Leu Ile Tyr Asn His Arg
1 5 10

<210> 77

<211> 10

<212> PRT

<213> Artificial

<220>

<223> binding 10 mer fragment L-form

<400> 77

Ser Thr Gly Arg Lys Val Phe Asn Arg Arg
1 5 10

<210> 78

<211> 11

<212> PRT

<213> Artificial

<220>

<223> binding 11 mer fragment L-form

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<400> 78

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg
1 5 10

<210> 79
<211> 8
<212> PRT
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<220>
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<400> 79

Asp Ser Asp Val Arg Arg Pro Trp
1 5

C1
<210> 80
<211> 8
<212> PRT
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<220>
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<400> 80

Ala Ala Asp Gln Arg Arg Gly Trp
1 5

<210> 81
<211> 8
<212> PRT
<213> Artificial

<220>
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<400> 81

Asp Gly Arg Gly Gly Arg Ser Tyr
1 5

<210> 82
<211> 4
<212> PRT
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<220>
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<400> 82

Arg Val Arg Ser
1

<210> 83
<211> 12
<212> PRT
<213> Artificial

Conc'd.
<220>
<223> binding 12 mer fragment L-form

<400> 83

Ser Val Arg Ser Gly Cys Gly Phe Arg Gly Ser Ser
1 5 10

<210> 84
<211> 11
<212> PRT
<213> Artificial

<220>
<223> binding 11 mer fragment L-form

<400> 84

Ser Val Arg Gly Gly Cys Gly Ala His Ser Ser
1 5 10